Comparison of the predicted amino acid sequence of the *T. aureum* probe 'TA-PKS-1-consensus' and the homologous region on ORF A of *Schizochytrium* PKS gene cluster (Accession number AAK72879).

Quality: 1269   Length: 525
Ratio: 2.469   Gaps: 10
Percent Similarity: 61.690   Percent Identity: 52.849

Match display thresholds for the alignment(s):
                | = IDENTITY
                : = 2
                . = 1

TA-PKS-1-consensus.pep x aak72879.genpept..

```
   1 LCKTLDLEWPH..VFARSIDIELGANEETAAQAIFEELSCPDLTVREAGY 48
     ||||: |||    ||.| :||  | . | || ||  |:.| |: :|| |
2277 LCKTIGLEWSESDVFSRGVDIAQGMHPEDAAVAIVREMACADIRIREVGI 2326

  49 TKDGKRWTTEARPVGLGKPKQALRSSDVFLVSGGARGITPVCVRELAKSI 98
     . .| |  |  .  | |.. :   || |||||||||||.|:||: : |
2327 GANQQRCTIRAAKLETGNPQRQIAKDDVLLVSGGARGITPLCIREITRQI 2376

  99 SGGTFVLLGRSPL.ADDPAWACGV.EEANIGTAAMAHLKAEFAAGRGPKP 146
     .|| ::|||||  . | :||| |: :|  :  ||  ||. |.|| ||||
2377 AGGKYILLGRSKVSASEPAWCAGITDEKAVQKAATQELKRAFSAGEGPKP 2426

 147 TPKAHKALVGSVLGAREVLGSLESIRAQGARAEYVSCDVSCAERVKAVVD 196
     ||:|   |||||||||||  |: .| | | :| | ||||. | |   |
2427 TPRAVTKLVGSVLGAREVRSSIAAIEALGGKAIYSSCDVNSAADVAKAVR 2476

 197 DLERRVGA.VTGVVHASGVLRDKSVERLELADFEVVYGTKVDGLLNLLQA 245
     | | ..|| |.|:|||||||||: :|:    :|: |:|||| || ||| |
2477 DAESQLGARVSGIVHASGVLRDRLIEKKLPDEFDAVFGTKVTGLENLLAA 2526

 246 VDRPKLRHLVLFSSLAGFHGNTGQAVYAMANEALNKMAFHLETAMPGLSV 295
     |||  |:|:|||||||||||| ||. ||||||||||   || |  .||
2527 VDRANLKHMVLFSSLAGFHGNVGQSDYAMANEALNKMG..LELA.KDVSV 2573

 296 KTIGFGPWDGGMVNDALKAHFASMGVQIIPLDGGAETVSRIIGACSPTQV 345
```

FIG.1A

```
        |.| |||||||||    ||  |  ||||||| :|||:||.||:   ||  ::
2574 KSICFGPWDGGMVTPQLKKQFQEMGVQIIPREGGADTVARIVLGSSPAEI 2623
              .           .           .           .           .
 346 LVGNWGLPPVVPNASVHKITVRLGGESANPFLSSHTIQGRKVLPMTXALG 395
        |||||  |      .    :  :: .| ||||  | ||||:||||| |:|
2624 LVGNWRTPSKKVGSDTITLHRKISAKS.NPFLEDHVIQGRRVLPMTLAIG 2672
              .           .           .           .           .
 396 LLAEAARGLYVGHQVXGIEDAQVFQGVVLDKGATCEVQLRRESSTASPSE 445
        |||   ||: |: .  |:|||.|.|| .|   ||| |     |||
2673 SLAETCLGLFPGYSLWAIDDAQLFKGVTVDGDVNCEVTL..TPSTAPSGR 2720
              .           .           .           .           .
 446 VVLSASLNVFAAGKVVPAYRAHVVIGASGPRTGGVQLELKDLGVDADPAC 495 .
        | . |.|   |..||.||||||| :||  |        ::   |  |||||
2721 VNVQATLKTFSSGKLVPAYRAVIVLSNQGAPPANATMQPPSL..DADPAL 2768
              .           .
 496 SVGKGALYDGRTLFHGPAFQYMDEV 520
          .|..|||:|||||||||. .|:|
2769 ...QGSVYDGKTLFHGPAFRGIDDV 2790
```

FIG.1B

Comparison of the predicted amino acid sequence of the *T. aureum* probe `TA-PKS-1-consensus` and the homologous region on ORF 5 of *Shewanella* PKS gene cluster (Accession number AAB81123).

Quality: 641   Length: 551
Ratio: 1,233   Gaps: 16
Percent Similarity: 47.379   Percent Identity: 39.919

Match display thresholds for the alignment(s):
                | = IDENTITY
                : =   2
                . =   1

TA--PKS-1-consensus.pep x aab81123.genpept


```
   1 LCKTLDLEWPHVFARSIDIELGANEETAAQAIFEELSCPDLTVREAGYTK 50
     | ||| ||| || |.:||   .   | || ||      . | | .
2094 LTKTLSHEWPQVFCRALDIATDVDATHLADAITSELFDSQAQLPEVGLSL 2143

  51 .DGK..RWTTEARPVGLGKPKQALRSSDVFLVSGGARGITPVCVRELAKS 97
     ||| | |   |          | | |.| ||.|||:|:| |   || |
2144 IDGKVNRVTLVAAEAADKTAKAELNSTDKILVTGGAKGVTFECALALA.S 2192

  98 ISGGTFVLLGRSPLADDPAWACGVEEANIGTAAMAHLKAEFAAGRGPKPT 147
     |   |:| ||| |   |.|| | : . : .||.||:        | |||
2193 RSQSHFILAGRSELQALPSWAEGKQTSELKSAAIAHI.....ISTGQKPT 2237

 148 PKAHKALVGSVLGAREVLGSLESIRAQGARAEYVSCDVSCAERVKAVVDD 197
     || .| | |  . |: .| .   || ||||| ||. .  : |
2238 PKQVEAAVWPVQSSIEINAALAAFNKVGASAEYVSMDVTDSAAITAA... 2284

 198 LERRVGAVTGVVHASGVLRDKSVERLELADFEVVYGTKVDGLLNLLQAVD 247
     | |   :||,:| .||| || ::   ||:   ||||||.|| || |.:
2285 LNGRSNEITGLIHGAGVLADKHIQDKTLAELAKVYGTKVNGLKALLAALE 2334

 248 RPKLRHLVLFSSLAGFHGNTGQAVYAMANEALNKMAFHLETAMPGLSVKT 297
     |:: | :||| |||:|| ||. |||.|: ||| |      |   | .
2335 PSKIKLLAMFSSAAGFYGNIGQSDYAMSNDILNKAALQFTARNPQAKVMS 2384

 298 IGFGPWDGGMVNDALKAHFASMGVQIIPLDGGAETVSRIIGACSPTQVLV 347
```
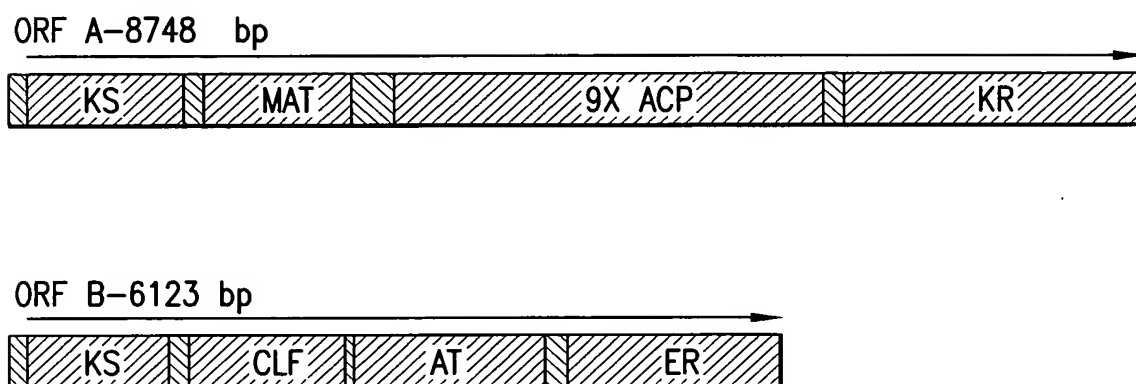
FIG.2A

```
        ·|||||||||  |||   |    || :|||  |||   ·  :  |  ·   |·|:
2385 FNWGPWDGGMVNPALKKMFTERGVYVIPLKAGAELFATQLLAETGVQLLI 2434
              ·           ·          ·        ·        ·
 348 G....................NWG..LPPVVPNASVHK.....IT.VRLG 369
     |                    | |  |   || |    |      :|  ||
2435 GTSMQGGSDTKATETASVKKLNAGEVLSASHPRAGAQKTPLQAVTATRLL 2484

              ·           ·          ·        ·        ·
 370 GESANPFLSSHTIQGRKVLPMTXALGLLAEAARGLYVGHQVXGIEDAQVF 419
        ||  |:  | | |  |||   |:  :  |||  : ·| ||  : |  ··
2485 TPSAMVFIEDHRIGGNSVLPTVCAIDWMREAASDM.LGAQVK.VLDYKLL 2532

              ·           ·          ·        ·        ·
 420 QGVVLDKGATCEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVV 469
     ·|:| :      |· | |  ·    | | | :·    |:  | |:|  ·:
2533 KGIVFETDEPQELTL..ELTPDDSDEATLQALIS..CNGR..PQYKATLI 2576

              ·           ·          ·        ·        ·
 470 LGASGPRTGGVQLELKDLGVDADPACSVGKGALYDGRTLFHGPAFQYMDE 519
        ·  :    | :|     ·  |  ·  |   ||   ||||||   |  ·
2577 SDNADIKQLNKQFDL......SAKAITTAK.ELYSNGTLFHGPRLQGIQS 2619

 520 V 520
     |
2620 V 2620
```

FIG.2B

Organization of PUFA–PKS genes from *Thraustochytrium aureum* ATCC 34304

ORF A–8748 bp

ORF B–6123 bp

KS=β–keto acyl synthase
MAT=MalonylCoA
transferase
ACP=Acyl carrier protein
KR=Ketoacyl–ACP reductase
AT=Acyl transferase

FIG.3

Sequence ID Nos. and Corresponding Sequences:

SEQ ID NO 1:
5'-AGC GGA TAA CAA TTT CAC ACA GG-3'

SEQ ID NO 2:
CACGAGGCCAAGCATTCGAGCAAAGCGCTCAACCAGCAGATCCCAGG
CGGGCGCGCCTGCTTCGTGGGCGTCTCGCGAATCGACGGACAGCTCG
GACTTAGCGGAGCTTGCGCGAAAGGAAAGGGCTGGGCTGAGGCCGCA
GAGATTGCTCAGCAAGGAGCCGTCGCAGGCTTGTGCAAGACCTTGGA
CCTAGAGTGGCCGCACGTCTTCGTCGCAGCATCGACATCGAGCTTGG
CGCGAACGAAGAAACAGCTGCGCAAGCAATCTTTGAGGAGCTCTCTT
GCCCGGACCTAACGGTGCGCGAAGCAGGATACACCAAAGACGGCAA
GCGGTGGACGACTGAGGCGCGACCGGTTGGGCTTGGCAAGCCCAGC
AGGCACTACGTTCTTCGGACGTCTTCTTGGTTTCTGGTGGGGCGCGGGG
AATTACACCTGTTTGCGTTCGCGAGTTGGCCAAATCGATCAGTGGTGG
CACTTTTGTCCTCCTCGGGCGGTCCCCTCTCGCTGATGATCCGGCGTGG
GCTTGCGGCGTCGAGGAAGCAAACATTGGGACAGCCGCTATGGCGCA
CCTCAAGGCCGAGTTCGCAGCCGGGCGCGGCCCGAAGCCGACGCCAA
AGGCCCACAAAGCACTCGTTGGGAGCGTCCTGGGGGCGCGCGAAGTC
CTTGGTTCGCTAGAGAGTATTCGCGCCCAGGGTGCGCGCGCCGAGTAC
GT

SEQ ID NO:3:
TCGCCAACACAAGTTCTGGTTGGCAACTGGGGCTTGCCCCCTGTAGTT
CCTAACGCGAGCGTGCACAAGATTACTGTGAGGCTTGGCGGGGAGTC
TGCAAACCCTTTCCTGTCCTCCCACACGATTCAAGGCAGAAAGGTCTT
GCCGATGACTGYGGCGCTTGGGCTTCTCGCTGAGGCGGCTCGAGGGCT
CTACGTCGGTCACCAAGTAGYCGGGATTGAGGACGCCCAAGTCTTCCA
GGGAGTCGTGTTGGACAAAGGGGCGACGTGTGAGGTCCAGCTTCGCC
GCGAGTCTTCGACTGCAAGCCCAAGCGAGGTTGTGCTGAGTGCTTCGC
TCAATGTATTCGCGGCGGGAAAGGTTGTGCCTGCGTACCGCGCGCATG
TCGTGCTCGGCGCTTCAGGGCCACGCACTGGCGGCGTGCAGCTTGAAC
TGAAAGATTTGGGCGTGGACGCCGACCCTGCTTGCTCCGTTGGCAAGG
GTGCGCTGTACGACGGTAGGACGCTGTTCCATGGGCCGGCGTTTCAGT
ACATGGATGAGGTTCCCTGGTGCTCGCCTGCAGAGCTTGCCGTGCGGT
GCCGTGTCGTTCCGAGCGCGGCTCAGGACCGCGGCCAATATGTTTCGC
GCGGAGTGTTGTACGACCCGTTCCTGAACGACACGGTGTTTCAAGCTC
TCCTTGTTTGGGCCCGTCTGGTCAGGGACAGCGCTTCGCTACCGAGCA
ACGTTGAACGAATCTCGTTCCACGGCCAGCCGCCGAGCGAGGGCGAG
GTGTAGTACACCACGCTCAAGCTGGACAGTGCTGCGAGCGGGCCGCT
CGACCCGATTGCAACAGGCGCATTTCTTCCTCCACCGAGCTTGCGGGG
CGGTCTTTGCATCAGGGCGAGCGAGTGTGGTTCTGAACAAGGCTCTTT
CGTATGATGGCTCTCGACCCAAAGGCGAGTAGAGTACTCTACTCAGTA

FIG.4-1

CTCCTTTTCACATACCGGCAGGCAGCGTTGCTGTGGGATGGCCGGGGG
CTCTTCTGCACGCGGCTCC

SEQ ID NO:4:
GAATTCGGCACGAGGCCGGCCTCACGACGCAGGTTGTTCGGTTCCGCG
CTGCAGGTCTGTCACGCAACGCGGACGGCTCTGTTCGAGTCCGCAACC
GCATCATCGGAAAGATTTCGCGCACGGAGCTCGCGGAGATGTTCATTC
GCCCCGCTCCGGAGGCCCTCTTGACCAAGTTGGTTGCGTCGGGTGAGA
TTTCGGCCGAGCAGMNGCCTGGCCAAACAAGTGCCGATGCCGACGAC
ATTGCCGTCGAGSAGAACTCGGGCGGCCACACGGACAATCGCCCGAT
CCATGTCATCCTTCCGCTGATCATCGCGCTCCGCAACAGGCTGCACAA
GGAGTGCGGTTACCCGGCGAGCCTTCGCGTTCGAGTTGGCGCGGGTGG
CGGGATCGGCTGCCCGCTTGCAGCAACTGCGGCCTTCAACATGGGCGC
CGCCTTTCTCGTGACAGGAACAGTCAACCAACTCAGCCGGCAGTCGG
GCACCTGCGACGCGGTGCGCATSAGCTTTTCAAAAGCGACCTACTCGG
ACATCACAATGGCGCCCGCCGCAGATATGTTTGACCAGGGGGTTGAG
CTCCAGGTGCTCAAGAAGGGCACCATGTTTCCGTCGCGCGCCAAGAA
GCTCTACGAGCTGTTTTGCACGTACAACTCGKTCGACGAGATGCCCGC
CGAGGAGCTCGCGCGGGTTGAGAAGCSGATYTTCCAAAAGCCCCTCG
CGGSCGTATGGGACGAGACGAAAGACTTTTACATCAACCGTCTCCACA
ACGAGGACAAGATCGAACGCGCAGAAAGGATGGCAAGCTCAAGAT
GTCGCTCTCGTTCCGCTGGTACCTTGGCCTGAGTTCGTTCTGGGCCAAC
AATGGAATCGCCGACCGCGTGCTGGACTATCAAGTGTGGTGCGGCCCT
GCGATTGGGGCCTGGAACGACTTTGCCAAGGGATCCTACCTCGACGCC
GAGGTCTGCGGCCAGTTTCCTTGCGTTGTGCAGGTCAACCTGCAGATC
CTCCACGCGCGGCCTACATGCAGCGCCTTCTGGCCGTCAAGCATGACC
CGCGCATCGAGTTTGACCTCGAGGACCCGGTCTTTGGTACGCCCCAC
TGCCGCGCTCTAAAGCGATGCAGCAACGCACTCTTTCGGAGGCCCGTC
GCTGCAGCACTTGTGCGAACTCGATAGGGTTTCTTTCAAGATTTCAATC
AACAAAACAAGTATTGGAATGACAAAAAAAAAAAAAAAACTCGAG

SEQ ID NO:5:
5'- CTT GTG CAA GAC CTT GGA CCT AGA G-3'

SEQ ID NO:6:
5'-GAA CCT CAT CCA TGT ACT GAA ACG C-3'

SEQ ID NO:7:
TTGTGCAAGA CCTTGGACCT AGAGTGGCCG CACGTCTTCG
CTCGCAGCATCGACATCGAG CTTGGCGCGA ACGAAGAAAC
AGCTGCGCAA GCAATCTTTGAGGAGCTCTC TTGCCCGGAC
CTAACGGTGC GCGAAGCAGG ATACACCAAAGACGGCAAGC
GGTGGACGAC TGAGGCGCGA CCGGTTGGGC TTGGCAAGCC
CAAGCAGGCA CTACGTTCTT CGGACGTCTT CTTGGTTTCT
GGTGGGGCGCGGGGAATTAC ACCTGTTTGC GTTCGCGAGT

FIG.4-2

TGGCCAAATC GATCAGTGGTGGCACTTTTG TCCTCCTCGG
GCGGTCCCCT CTCGCTGATG ATCCGGCGTGGGCTTGCGGC
GTCGAGGAAG CAAACATTGG GACAGCCGCT ATGGCGCACC
TCAAGGCCGA GTTCGCAGCC GGGCGCGGCC CGAAGCCGAC
GCCAAAGGCCCACAAAGCAC TCGTTGGGAG CGTCCTGGGG
GCGCGCGAAG TCCTTGGTTCGCTAGAGAGT ATTCGCGCCC
AGGGTGCGCG CGCCGAGTAC GTTTCCTGCGACGTTCGTG
TGCGGAGCGC GTCAAGGCCG TCGTCGACGA TCTCGAGCGA
CGGGTCGGGG CTGTAACTGG GGTTGTGCAC GCCTCTGGTG
TTCTCCGAGACAAGTCCGTT GAGCGCTTGG AGCTCGCCGA
CTTCGAGGTC GTGTACGGCACCAAGGTGGA CGGCCTGCTC
AACCTGCTGC AGGCCGTGGA CCGCCCCAAACTCCGGCACT
TGGTCCTCTT CAGCTCCCTG GCCGGTTTCC ACGGCAACAC
TGGGCAGGCC GTGTACGCTA TGGCGAATGA GGCGCTGAAC
AAGATGGCCTTCCATTTGGA AACTGCGATG CCTGGCCTCT
CGGTCAAGAC GATCGGGTTTGGACCTTGGG ACGGCGGCAT
GGTCAACGAT GCGCTGAAAG CGCACTTTGCGTCTATGGGC
GTCCAAATTA TTCCGCTCGA CGGYGGCGCG GAGACCGTTT
CCCGAATCAT CGGGGCGTGC TCGCCAACAC AAGTTCTGGT
TGGCAACTGGGGCTTGCCCC CTGTAGTTCC TAACGCGAGC
GTGCACAAGA TTACTGTGAGGCTTGGCGGG GAGTCTGCAA
ACCCTTTCCT GTCCTCCCAC ACGATTCAAGGCAGAAAGGT
CTTGCCGATG ACTGYGGCGC TTGGGCTTCT CGCTGAGGCG
GCTCGAGGGC TCTACGTCGG TCACCAAGTA GYCGGGATTG
AGGACGCCCAAGTCTTCCAG GGAGTCGTGT TGGACAAAGG
GGCGACGTGT GAGGTCCAGCTTCGCCGCGA GTCTTCGACT
GCAAGCCCAA GCGAGGTTGT GCTGAGTGCTTCGCTCAATG
TATTCGCGGC GGGAAAGGTT GTGCCTGCGT ACCGCGCGCA
TGTCGTGCTC GGCGCTTCAG GGCCACGCAC TGGCGGCGTG
CAGCTTGAACTGAAAGATTT GGGCGTGGAC GCCGACCCTG
CTTGCTCCGT TGGCAAGGGTGCGCTGTACG ACGGTAGGAC
GCTGTTCCAT GGGCCGGCGT TTCAGTACATGGATGAGGTT C

SEQ ID NO:8:
CGCAAGTGCATCCGGCCATCATTGGGCCATCATTGGGCCATCATTGGT
GTTTTGGGCCGCGCTTTGCGGATCGTCCGGCCGATCAGGTACGAGGCC
ACGAACCTACGTCGTTTGCCGCGCTCAGGCTGGTTGGTTGCACTTGGA
CTCTTCTGTGACCTTTCATCGTGTGCAGGCAAACTCGATTTGCAGACCC
GAGACACGGCGAAGGATCCGTGCTGCAAACGCAAGTGGAGTGCGTCG
AGAGCACCGCCGAGACCAAGAGCCGAGGCAGACAAGGCCAGCAACG
AGATGGAGACAAAGGACGATCGCGTTGCGATCGTGGGCATGTCGGCC
ATACTGCCTTGCGGTGAGTCAGTGCGCGAGTCGTGGGAGGCGATTCGC
GAGGGGCTCGATTGCCTGCAGGACCTGCCTGCGGACCGAGTCGATAT
CACGGCGTACTACGACCCGAACAAGACAACCAAGGACAAGATCTACT
GCAAGCGCGGCGGCTTCATTCCCGAGTATGACTTTGACGCGCGCGAGT

FIG.4-3

TCGGCCTCAACATGTTCCAGATGGAGGACTCGGACGCCAACCAAACC
GTGACTTTGCTCAAGGTCAAGGAGGCTCTCGAGGACGCCGGGGTGGA
GCCCTTCACAAAGAAGAAGAAGAACATTGGCTGCGTGCTCGGCATCG
GCGGCGGGCAGAAGGCGAGCCACGAGTTTTACTCCCGACTCAACTAT
GTGGTCGTGGAGAAGGTGCTTCGCAAGATGAACCTCCCCGACGAGGT
TGTCGAGGCCGCCGTCGAAAGTACAAGGCCAACTTTCCTGAATGGC
GCCTCGACTCGTTCCCTGGGTTTCTTGGCAACGTGACCGCCGGGCGGT
GCAGCAACGTCTTCAACATGGAAGGCATGAACTGCGTCGTGGACGCT
GCGTGCGCCAGCTCGCTCATCGCGATCAAGGTTGCCATTGATGAGCTC
CTCCACGGGGACTGCGACACCATGATTGCCGGTGCGACCTGCACCGA
CAACTCGATCGGGATGTACATGGCCTTTTCCAAAACCCCAGTTTTCTCC
ACCGACCAGAGCGTCAAGGCGTACGACGCCAAGACGAAAGGCATGC
TCATCGGCGAAGGCTCGGCCATGGTCGTGCTCAAGCGGTACGCGGAC
GCCGTTCGGGATGGTGATGAGATCCATGCCGTCATCAGGGCATGCGCC
TCGTCCAGCGACGGCAAGGCTGCTGGCATTTACGCACCGACGGTGTCG
GGTCAAGAAGAGGCACTGCGGCGCGCGTACGCCCGAGCTGGCGTGGA
CCCCTCCACCGTCACGCTGGTGGAGGGCCACGGCACTGGCACACCCG
TCGGGGACCGGATTGAGCTGACCGCCTTGCGCAACGTCTTTGACGCAG
CCAACAAAGGCCGCAAGGAAACAGTCGCGGTGGGAAGCATCAAGTC
GCAGATCGGTCACCTGAAGGCCGTGGCCGGCTTTGCCGGTCTCGTCAA
GGTTGTCATGGCCCTCAAGCACAAGACGCTGCCGCAGACCATCAACG
TTCACGACCCGCCCGCACTGCACGACGGCTCGCCCATCCAGGATTCGA
GTCTTTACATCAACACGATGAACCGGCCCTGGTTTACGGCACCTGGCG
TCCCCCGCCGTGCAGGCATCTCTAGCTTTGGGTTTGGCGGCGCCAACT
ACCACGCTGTTCTCGAAGAGGCCGAGCCTGAGCACGCGAAGCCGTAT
CGCATGAACCAAGTTCCAACAACCGGTGCTCTTGCACGCAAGCTCCGCG
TCAGCTCTTGCCTCCATCTGCGACGCTCAGGCCGACGCGCTCCAGGCC
GCCGTCTCGCCCGAAGCCAGCAAGCACGCAGACTACCGCGCCATCGT
AGCGTTCCATGAAGCGTTTAAGCTTCGCGCTGGAGTGCCGGCCGGCCA
TGCTCGAATTGGCTTTGTGTCCGGCAGCGCGGCAGCAACGCTTGCAGT
GCTCCGAGCCGCCTCTGCAAAACTCAAGCAGTCGAGTGCGACGCTCG
AATGGACCCTGCTCCGCGAGGGCGTCACGTACCGCTCCGCCGCGATG
CACACTCCTGGCAGTGTCGCTGCTCTGTTTGCCGGGCAAGGCGCGCAG
TACACGCACATGTTCGCTGACGTTGCCATGAACTGGCCACCGTTTCGA
AGCGCCGTGCAAGAGATGGATGCCGCTCAAGTCACGGCGGCAGCGCC
GAAGCGCCTCAGCGAGGTCCTGTATCCGCGCAAGCCGTACGCTGCAG
AGCCCGAGCAAGACAACAAGGCCATCTCGATGACGATTAACTCGCAA
CCGGCCCTCATGGCCTGCGCTGCTGGGGCGTTTGAGGTGTTTCGTCAA
GCTGGTCTTGCGCCCGACCACGTCGCGGGTCATTCTCTCGGCGAGTTT
GGTGCTTTGCTCGCCGCTGGATGCGCAAGCCGTGAGGAGCTCTTCCGT
CTGGTCTGCAGCAGAGCGAAGGCAATGCAAGACGTTCCCAAGCCAAG
CGAGGGCGTCATGGCAGCTGTCATCGGCCGTGGTGCTGACAAGCTCA
CGCTGCAAGGCGATGGTGCGTGGCTTGCCAACTGCAACTCGCCAAGC
CAAGTGGTCATTTCCGGCGACAAGACTGCTGTCGAGCGTGAATCCAGC
CGGTTGGCAGGCCTTGGCTTCAGGATCATTCCGCTTGCATGCGAAGGC

FIG.4-4

GCCTTCCATTCACCGCACATGACGGCGGCCCAGGCCACGTTTCAGGCT
GCACTGGACAGCCTCAAGATCTCCACCCCGACGAACGGGGCGCGCCT
·GTACAACAACGTTTCCGGAAAGACCTGCCGATCCCTGGGTGAACTCC
GCGACTGCCTGGGCAAGCACATGACAAGTCCTGTGCTCTTCCAGGCAC
AGGTAGAGAACATGTACGCTGCCGGGGCGCGCATTTTCGTGGAGTTTG
GCCCGAAGCAAGTCCTCTCCAAGCTCGTAGGCGAGATTCTCGCCGAC
AAGTCAGACTTTGTGACAGTCGCGGTCAACTCGTCATCGTCCAAGGAC
AGCGACGTGCAACTTCGTGAAGCTGCTGCGAAGCTCGCGGTCCTTGGC
GTCCCGTTGGCGAACTTTGACCCTTGGGAGCTCTGCGACGCGCGGCGT
CTTCGCGAATGCCCGCGATCCAAGACGACGTTGCGCTTGTCTGCAGCG
ACCTACGTGTCGAACAAGACCCTTGCTGCTAGGGAGAAGGTCATGGA
GGACAACTGCGACTTTTCTTCGCTCTTTGCCTCCGGTCCAGCAAGCCA
AGAGATGGAGCGAGAAATAGCCAACCTTCGCGCTGAGCTGGAGGCGG
CCCAACGCCAGCTTGACACGGCCAAAACCCAGCTTGCTCGAAAGCAA
GTGCAGGACCCCACCGCTGACCGACAGCGCGATATGATTGCCAAGCA
CCGATCCACACTCGCAGCAATGGTGAAGGAATTCGAGGCTCTGGCAA
GTGGTAGTCCTTGCGCTGTTCCGTTTGCGCCTGTGGTGGACACTGCTGT
CGAAGACGTGCCTTTTGCGGACAAGGTCTCGACGCCACCGCCCCAAG
TCACTTCCGCTCCCATCGCCGAGCTCGCGCGCGCCGAGGCCGTCGTCA
TGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAG
GCCGACATGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCG
CATTGAGATCCTGGCAGCTGTCCAGGCCCAGCTCGGGGTCGAGGCCA
AGGACGTCGACGCGCTCAGCCGCACACGAACAGTTGGCGAGGTCGTT
GACGCCATGAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCGCCTTC
GCCGATGGCCCAGCCCCAAGCCTCAGCACCATCACCGTCCCCTACTGC
CTCTGTGCTGCCTAAGCCTGTTGCTTACCAGCTAGTGTCGATCCCGCC
AAGCTCGCGCGCGCCGAAGCGGTCGTCATGGAGGTTCTCGCCGCCAA
GACTGGCTACGAGGTCGACATGATCGAGGCTGACATGCTGCTCGACG
CCGAGCTCGGCATCGACTCGGTCAAGCGCATTGAGATCCTGGCGGCTG
TCCAAGCTCAGCTCGGGGTCGAGGCCAAGGATGTCGACGCGCTCAGC
CGCACACGCACTGTTGGCGAGGTCGTTGATGCCATGAAGGCTGAGAT
CGGCGGGCAAGCGACCAGCGCACCTGCGTCCGTGGCCCAGCCCCAAG
CCTCAGCACCATCACCGTCCGCAACAACTGCCTCTGTGCTGCCTAAGC
CTGTTGCTGCACCAACTAGCGCCGATCCCGCCAAGCTCGCGCGCGCCG
AAGCCGTCGTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCG
ACATGATCGAGGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGACT
CGGTCAAGCGCATTGAGATCCTGGCGGCTGTCCAAGCCCAGCTCGGG
GTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACACGCACGGTTGG
CGAGGTCGTCGAGGCCATGAAGGCTGAGATCGGCGGGCAAGCGACC
AGTGCACCTGCGTCCGTGGCCCAGCCCCAAATCTCTGTGTCCCCTACG
CCTCTCGCTGCATCTCCTAGTGCCGATCCTGCCAAGCTCGCGCGCGCC
GAAGCCGTCGTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTC
GACATGATCGAGGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGA
CTCCGTCAAGCGCATCGAGATCCTGGCGGCTGTCCAGGCCCAGCTCGG
GGTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACACGCACTGTTG

FIG.4-5

GCGAGGTCGTTGACGCCATGAAGGCTGAGATCGGCGGGCAAGCGACC
AGTGCGCCTGCATCCGTGGCCCAGCCCCAAGCCTCAGCACCGTCGCC
GTCCGCTACTGCCTCTGTGCTGCCTAAGCCTGTTGCTGCACCAACTAGC
GCCGATCCCGCCAAGCTCGCGCGCGCCGAAGCCGTCGTCATGGAGGT
TCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAGGCTGACAT
GCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCGCATCGAGA
TCCTGGCGGCTGTCCAAGCCCAGCTCGGGGTCGAGGCCAAGGACGTC
GACGCGCTCAGCCGCACACGCACGGTTGGCGAGGTCGTCGAGGCCAT
GAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCACCTGCGTCCATGG
CCCAGCCCCAAATCTCTGTGTCCCCTACGCCTCTCGCTGCATCTCCTAG
TGCCGATCCTGCCAAGCTCGCGCGCGCCGAGGCCGTCGTCATGGAGGT
TCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCGAGGCCGACA
TGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAAGCGCATCGAG
ATCCTGGCGGCTGTCCAAGCTCAGCTCGGGGTCGAGGCCAAGGACGT
CGACGCGCTCAGCCGCACACGCACGGTTGGCGAGGTCGTTGATGCCA
TGAAGGCTGAGATCGGCGGGCAAGCGACCAGTGCGCCTGCATCCGTG
GCCCAGCCCCAAGCCTCAGCACCGTCGCCGTCCGCTACTGCCTCTGCG
CCTGTTACGCCTCTCGCTGCACCAGCTAGTGTCGATCCCGCCAAGCTC
GCGCGCGCCGAAGCCGTCGTCATGGAGGTTCTCGCCGCCAAGACTGG
CTACGAGGTCGACATGATCGAGGCTGACATGCTGCTCGACGCCGAGC
TCGGCATCGACTCCGTCAAGCGGATTGAGATCCTGGCGGCTGTCCAAG
CCCAGCTCGGGGTCGAGGCCAAGGACGTCGACGCGCTCAGCCGCACA
CGCACTGTTGGCGAGGTCGTTGACGCCATGAAGGCTGAGATCGGCGG
GCAAGCGACCAGCGCACCTGCGTCCGTGGCCCAGCCCCAAGCCTCAG
CACCGTCGCCGTCCGCTACTGCCTCTGTGCTGCCTAAGCCTGTTGCTTC
ACCAGCTAGTGTCGATCCCGCCAAGCTCGCGCGCGCCGAAGCGGTCG
TCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATCG
ACGCTGACATGCTGCTCGACGCCGAGCTCGGCATCGACTCCGTCAAGC
GCATCGAGATCCTGGCGGCTGTCCAAGCCCAGCTCGGGGTCGAGGCC
AAGGACGTCGACGCGCTCAGCCGCACACGAACGGTTGGCGAGGTCGT
CGAGGCCATGAAGGCTGAGATCGGGGCAGCAGGTCCAAACGATGCA
CAAGCAGCGTCTGGGCATCTCTTTGGCACGGGATGTGAAGACCTGAG
CCTTTGCTCTGCTTCTGTGGTTGAGATTGCTCGTTGCAGCGAACTAGCT
CTGGAGCGCCCGATGGATCGGCCCATTCTTATTGTAAGCGATGGATCA
GCATTGCCGGCGGCTCTGGCTAGTCGACTGGGGTCGTGTGCAGTAATC
CTCACGACCGCAGGCGAGACCGACCAATCTGTGCGCTCGACGAAGCA
CGTTGACATGGAAGGGTGGGGCGAGGCAGATCTCGTGCGCGCTCTTG
AAGCAGTAGAGTCTCGATTCGGCGTCCCAGGCGGCGTCGTGGTGCTTG
AGCGCGCCTCAGAAACAGCTAGGGACCAGCTTGGCTTTGCCCTGCTGC
TTGCCAAGCATTCGAGCAAAGCGCTCAACCAGCAGATCCCAGGCGGG
CGCGCCTGCTTCGTGGGCGTCTCGCGAATCGACGGAAAGCTCGGACTT
AGCGGAGCTTGCGCGAAAGGAAAGGGCTGGGCTGAGGCCGCAGAGA
TTGCTCAGCAAGGAGCCGTCGCGGGCTTGTGCAAGACCTTGGACCTAG
AGTGGCCGCACGTCTTCGCTCGCAGCATCGACATCGAGCTTGGCGCGA
ACGAAGAAACAGCTGCGCAAGCAATCTTTGAGGAGCTCTCTTGCCCG

FIG.4-6

GACCTAACGGTGCGCGAAGCAGGATACACCAAAGACGGCAAGCGGT
GGACGACTGAGGCGCGACCGGTTGGGCTTGGCAAGCCCAAGCAGGCA
CTACGTTCTTCGGACGTCTTCTTGGTTTCTGGTGGGGCGCGGGGAATTA
CACCTGTTTGCGTTCGCGAGTTGGCCAAATCGATCAGTGGTGGCACTTT
TGTCCTCCTCGGGCGGTCCCCTCTCGCTGATGATCCGGCGTGGGCTTGC
GGCGTCGAGGAAGCAAACATTGGGACAGCCGCTATGGCGCACCTCAA
GGCCGAGTTCGCAGCCGGGCGCGGCCCGAAGCCGACGCCAAAGGCC
CACAAAGCACTCGTTGGGAGCGTCCTGGGGGCGCGCGAAGTCCTTGG
TTCGCTAGAGAGTATTCGCGCCCAGGGTGCGCGCGCCGAGTACGTTTC
CTGCGACGTTTCGTGTGCGGAGCGCGTCAAGGCCGTCGTCGACGATCT
CGAGCGACGGGTCGGGGCTGTAACTGGGGTTGTGCACGCCTCTGGTGT
TCTCCGAGACAAGTCCGTTGAGCGCTTGGAGCTCGCCGACTTCGAGGT
CGTGTACGGCACCAAGGTGGACGGCCTGCTCAACCTGCTGCAGGCCG
TGGACCGCCCCAAACTCCGGCACTTGGTCCTCTTCAGCTCCCTGGCCG
GTTTCCACGGCAACACTGGGCAGGCCGTGTACGCTATGGCGAATGAG
GCGCTGAACAAGATGGCCTTCCATTTGGAAACTGCGATGCCTGGCCTC
TCGGTCAAGACGATCGGGTTTGGACCTTGGGACGGCGGCATGGTCAA
CGATGCGCTGAAAGCGCACTTTGCGTCTATGGGCGTCCAAATTATTCC
GCTCGACGGCGGCGCGGAGACCGTTTCCCCGAATCATCGGGGCGTGCT
CGCCAACACAAGTTCTGGTTGGCAACTGGGGCTTGCCCCCTGTAGTTC
CTAACGCGAGCGTGCACAAGATTACTGTGAGGCTTGGCGGGGAGTCT
GCAAACCCTTTCCTGTCCTCGCACACGATTCAAGGCAGAAAGGTCTTG
CCGATGACTGTGGCGCTTGGGCTTCTCGCTGAGGCGGCTCGAGGGCTC
TACGTCGGTCACCAAGTAGTCGGGATTGAGGACGCCCAAGTCTTCCAG
GGAGTCGTGTTGGACAAAGGGGCGACGTGTGAGGTCCAGCTTCGCCG
CGAGTCTTCGACTGCAAGCCCAAGCGAGGTTGTGCTGAGTGCTTCGCT
CAATGTATTCGCGGCGGGAAAGGTTGTGCCTGCGTACCGCGCGCATGT
CGTGCTCGGCGCTTCAGGGCCACGCACTGGCGGCGTGCAGCTTGAACT
GAAAGATTTGGGCGTGGACGCCGACCCTGCTTGCTCCGTTGGCAAGGG
TGCGCTGTACGACGGTAGGACGCTGTTCCATGGGCCGGCGTTTCAGTA
CATGGATGAGGTTCTCGGTGCTCGCCTGCAGAGCTTGCCGTGCGGTG
CCGTGTCGTTCCGAGCGCGGCTCAGGACCGCGGCCAATTTGTTTCGCG
CGGAGTGTTGTACGACCCGTTCCTGAACGACACGGTGTTTCAAGCTCT
CCTTGTGGGCCCGTCTGGTCAGGGACAGCGCTTCGCTACCGAGCAA
CGTTGAACGAATCTCGTTCCACGGCCAGCCGCCGAGCGAGGGCGAGG
TGTTTTACACCACGCTCAAGCTGGACAGTGCTGCGAGCGGGCCGCTCG
ACCCGATTGCAAAGGCGCAGTTCTTCCTCCACCGAGCTTGCGGGGCGG
TCTTTGCATCAGGGCGAGCGAGTGTGGTTCTGAACAAGGCTCTTTCGTT
TTGA

SEQ ID NO:9:
CAAGCAATCGGCCATCGAGCTGCGCGTTGGAGCTGCCGATCGAAATC
GAAAGCAAGAGGCCACAAGGCTCAGAAAGAGATGAACCAGGGCGGG
AGAAATGACGAGGGCGTCTCGGTGGCGCGCGCGGACCCATGCCCTGA
CACGCGGATCGCTGTCGTGGGCATGGCGGTCGAGTATGCAGGGTGCC

FIG.4-7

GCGGCAAGGAAGCGTTCTGGGACACGCTCATGAACGGCAAAATCAAC
TCTGCCTGTATCTCAGACGATCGCCTCGGGTCAGCACGACGAGAAGA
GCACTATGCGCCCGAGAGGTCAAAGTACGCCGATACGTTCTGCAACG
AGAGGTACGGATGCATCGATCCCAAAGTCGACAACGAGCACGACCTG
CTCCTCGGCCTCGCCGCGGCTGCGCTTCAAGACGCGCAGGACAGGCG
CAGCGACGGCGGCAAGTTCGACCCAGCGCAGCTCAAGCGCTGCGGCA
TTGTCAGCGGCTGCCTGTCCTTCCCGATGGACAACCTGCAAGGCGAGC
TGCTCAACCTTTACCAAGCCCATGCTGAGAGGCGGATTGGCAAGCATT
GCTTCGCGGACCAAACGCCCTGGTCGACGCGAACCAGAGCGCTTCAC
CCGCTGCCCGGGGACCCGAGGACCCACCGCGACCCAGCCTCCTTCGT
CGCCGGACAGCTCGGCCTCGGCCCGCTGCACTACTCGCTCGACGCCGC
CTGCGCCTCGGCCCTTTACGTTCTGCGACTCGCTCAGGACCACCTCCTC
TCGGGCGAGGCTGACTTGATGCTGTGCGGAGCGACGTGCTTCCCAGAG
CCCTTCTTCATCCTGACTGGGTTTAGCACGTTCCACGCGATGCCAGTCG
GTGAGAACGGTGTCTCGATGCCGTTTCATCGGGACACGCAAGGGCTG
ACGCCCGGCGAGGGCGGCTCGGTGATGGTGCTCAAGCGCCTCGCGGA
CGCCGAGCGCGACGGAGACCACATCTACGGGACGCTTCTTGGAGCCA
GCTTGAGCAACGCAGGCTGCGGGCTTCCTCTCAAGCCGCACCAGCCA
AGCGAGGAGGCCTGCTTGAAAGCCACCTACGAGCTCGTCGGCGTGCC
GCCCCGAGACGTCCAGTACGTCGAGTGCCACGCCACCGGCACGCCGC
AGGGCGACACCGTCGAGCTCCAAGCCGTCAAAGCCTGCTTTGAGGGC
GCAAGCCCCCGGATCGGGTCCACGAAAGGCAACTTCGGACACACCCT
CGTCGCGGCCGGCTTTGCGGGAATGTGCAAGGTTCTCCTTGCAATGGA
GCGCGGCGTGATCCCCCCGACCCCGGGCGTTGACTCTGGCACCCAGAT
TGATCCCCTCGTCGTCACAGCGGCGCTCCCGTGGCCGGATACGCGCGG
CGGGCCGAAACGCGCAGGACTCTCCGCATTCGGATTCGGGGGCACAA
ACGCGCACGCCGTCTTTGAGGAGCATATTCCCTCGAGAGCTCCGCCCG
CAGTACTCTGCCAGCCTCGCCTCGGCAGCGGACCAAACCGAAAGCTT
GCTATCGTCGGCATGGATGCCACGTTTGGATCCTTGAAGGGTCTCTCC
GCACTAGAAGCTGCGCTTTACGAGGCAAGGCACGCTGCGCGGCCCCT
GCCTGCGAAGCGCTGGCGCTTCTTGGGCGGGGACGAGTCCTTTCTCCA
CGAGATCGGACTCGAGTGCTCTCCGCACGGGTGCTACATTGAGGACGT
GGATGTGGACTTTAAGCGACTCCGCACGCCAATGGTGCCGGAGGACT
TGCTCCGGCCGCAACAGCTCCTGGCCGTGTCGACGATTGACAAGGCC
ATCCTCGACTCGGGCTTGGCCAAGGGCGGCAACGTGGCTGTCCTTGTC
GGCCTCGGGACGGACCTCGAGCTCTACCGCCACCGAGCTCGGGTTGC
GCTTAAGGAGCGTCTTCAAGGACTGGTTCGCTCTGCCGAGGGAGGAG
CCCTGACGTCTCGCCTGATGAACTATATCAATGATAGCGGAACGTCGA
CCTCCTACACGTCGTATATCGGCAACCTCGTCGCCACGCGCGTCTCGT
CCCAGTGGGGCTTCACTGGGCCGTCGTTCACCGTCACGGAAGGGGCC
AACTCGGTCCATCGGTGCGCCCAGCTCGCCAAGTACATGCTCGACCGC
GGCGAGGTCGACGCCGTCGTGGTTGCAGGAGTCGACCTGTGCGGGAG
CGCCGAGGCGTTCTTCGTGAGGTCGCGCCGCATGCAGATCTCGAAAA
GTCAGCGCCCGGCCGCGCCGTTTGACCGCGCCGCAGACGGCTTCTTCG
CGGGGGAAGGGTGCGGCGCCCTCGTCTTCAAACGCCTGACTGACTGT

FIG.4-8

GTGTCTGGCGAGCGAATCTACGCGTCCCTCGACTCGGTCGTCGTCGCA
ACCACGCCGCGCGCCGCTCTTCGTGCTGCCGCAGGGTCGGCGCGGGTT
GACCCAGCCAGCATCGACATGGTCGAGCTGAGCGCAGATTCCCACCG
GTTTGTGCGGGCGCCAGGCACCGTGGCTCAGCCTCTGACAGCCGAAGT
CGAGGTCGGGGCGGTGCGGGAAGTGATCGGGACCGCGGGGAGGGGC
TCTCGAAGCGTGGCCGTCGGATCGGTCCGCGCCAACGTCGGGGACGC
AGGGTTTGCTTCCGGGGCCGCTGCCCTCGTAAAAACTGCGCTCTGCTT
GCACAACCGCTACTTGGCGGCTACCCCAGGCTGGGATGCGCCTGCTGC
CGGCGTGGATTTTGGTGCCGAGCTGTACGTTTGCCGCGAGTCGCGTGC
TTGGGTCAAGAACGCCGGCGTTGCACGGCACGCCGCAATTTCTGGCGT
GGACGAAGGCGGGTCGTGCTATGGGCTGGTTCTTTCGGACGTGCCTGG
GCAGTACGAGACCGGCAACCGCATCTCCCTCCAGGCCGAGTCGCCCA
AGCTCTTGCTCCTCTCGGCTCCAGACCACGCCGCCTTGCTGGACAAGG
TGGCGGCCGAGCTCGCAGCCCTTGAGCAAGCCGACGGCTTGAGCGCC
GCCGCGGCTGCCGTAGACCGCTTACTCGGCGAGTCGCTCGTCGGTTGC
GCGGCTGGCAGCGGCGGGCTGACCCTTTGCTTGGTGGCTTCGCCTGCC
AGCCTCCACAAGGAGCTTGCGCTGGCCCATCGAGGGATCCCGCGCTG
CATCAAAGCACGGCGCGACTGGGCCAGCCCGGCAGGGAGCTACTTCG
CCCCGGAGCCGATCGCAAGCGACCGCGTCGCGTTCATGTACGGGGAA
GGACGAAGCCCGTACTGCGGCGTCGGCCGCGACCTCCACCGGATCTG
GCCCGCGCTGCATGAGCGGGTGAACGCCAAGACTGTCAACCTCTGGG
GTGACGGTGACGCCTGGCTGCTGCCACGTGCAACCTCGGCCGAGGAA
GAGGAGCAACTCTGCCGCAACTTCGACTCGAACCAGGTTGAGATGTTT
CGAACGGGCGTGTACATCTCGATGTGCTTGACCGACCTCGCTCGAAGC
TTGATTGGACTGGGCCCTAAGGCGAGCTTTGGGCTCAGCCTAGGCGAG
GTTTCCATGCTCTTCGCTCTGAGCGAGTCCAACTGTAGACTGTCGGAG
GAAATGACCCGCAGGCTCCGTGCGTCCCCGGTGTGGAACTCGGAGCT
CGCCGTCGAGTTCAACGCCCTTCGAAAGTTGTGGGGGGTCGCGCCGGG
GGCACCCGTCGACTCGTTCTGGCAAGGTTATGTCGTGCGCGCAACGCG
GGCTCAGGTGGAGCAAGCCATTGGGGAGGACAATCAGTTTGTGCGTC
TCCTGATCGTGAACGACTCGCAATCAGTCCTGATCGCCGGCAAGCCGG
CGGCGTGCGAAGCCGTAATTGCTCGCATCGGGTCTATTCTTCCCCCGCT
GCAAGTGTCGCAAGGCATGGTGGGGCACTGTGCCGAGGTCTTGCCGT
ACACGAGCGAGATCGGGCGCATCCACAACATGCTTCGCTTCCCATCGC
AGGACGAAACGGGCGGTTGCAAAATGTACTCTAGCGTCTCAAACTCG
CGCATCGGGCCAGTCGAGGAGAGCCAGATGGGCCCAGGCACTGAGCT
CGTTTTCTCGCCGTCAATGGAAGACTTTGTCGCCCAGCTGTACTCGCGA
GTTGCAGACTTTCCGGCGATCACCGAGGCGGTTACCAGCAGGGTCAT
GACGTGTTTGTCGAAGTGGGGCCGGACCATTCACGGTCGGCTGCTGTC
CGCTCCACGCTTGGACCCACTCGGCGACACATCGCTGTGGCGATGGAC
CGCAAGGGTGAGTCAGCTTGGTCGCAGCTTCTGAAAATGCTGGCTACG
CTTGCGTCGCACCGCGTGCCGGGCCTGGACCTTTCATCCATGTACCAC
CCCGCAGTGGTGGAGCGTTGCAGGCTGGCGCTGGCAGCACAACGATC
GGGCCAGCCAGAGCAGCGGAACAAGTTTTTGCGCACGATAGAGGTGA
ATGGGTTCTACGACCCGGCCGACGCGACCATCCCTGAGGCCGTCGCA

FIG.4-9

ACAATTCTGCCGGCAACTGCTGCGATTTCGCCTCCAAAGCTTGGCGCT
CCGCACGACTCGCAACCCGAGGCGGAGGCTCGCCCCGTGGGCGAGGC
CTCTGTGCCAAGGCGGGCCACGAGCTCGAGCAAATTGGCCAGGACGC
TTGCCATCGATGCTTGCGACTCCGACGTGCGCGCCGCCTTGCTGGACC
TGGACGCGCCAATCGCGGTCGGCGGCTCCTCGCGCGCCCAAGTCCCG
CCGTGCCCAGTGAGCGCGCTCGGAAGCGCCGCCTTTCGAGCGGCACA
CGGCGTCGATTATGCGCTCTACATGGGCGCAATGGCCAAAGGCGTCG
CGTCAGCGGAGATGGTCATCGCTGCTGGCAAGGCCCGCATGCTCGCGT
CATTTGGCGCGGGGGGGCTTCCCCTGGGCGAGGTCGAAGAGGCGTTG
GACAAGATCCAGGCCGCTCTGCCCGAGGGGCCGTTCGCCGTCAACCT
CATTCACTCGCCGTTCGATCCAAACCITGAGGAGGGCAACGTCGAGCT
GTTCCTGAGGCGCGGTATCCGGCTGGTCGAGGCCTCTGCGTTCATGTC
GGTCACGCCGTCGTTGGTGCGCTACCGAGTCGCCGGACTCGAGCGAG
GCCCTGGCGGGACCGCCCGAGTGCTGAACCGCGTGATTGGCAAGGTG
AGCCGTGCGGAGCTCGCAGAAATGTITATGCGGCCGCCTCCCGCCGCG
ATCGTCTCCAAGCTCCTCGCCCAGGGCCTGGTCACTGAGGAGCAGGC
GTCACTTGCAGAGATCGTCCCACTGGTTGACGACGTTGCAATCGAAGC
CGACTCGGGCGGTCACACAGACAACCGCCCGATCCACGTCGTTTTGCC
CGTCGTCCTCGCGCTGCGAGACCGCGTCATGCGTGAGTGCAAGTATCC
AGCCGCCAATCGCGTCCGCGTGGGCGCCGGAGGCGGGATCGGCTGCC
CTGCCGCGGCGCGAGCTGCGTTCGACATGGGCGCAGCATTCGTTCTCA
CGGGCTCGATCAACCAGCTCACGCGCCAGGCTGGGACGAGCGACAGC
GTGCGTGCTGCCCTTGCACGCGCGACCTACTCGGACGTGACAATGGCC
CCGGCGGCCGATATGTITGACCAGGGCGTCAAGCTGCAGGTCTTGAAG
CGCGGCACGATGTTCCCGGCGCGCGCAAACAAGCTGTACGAGTTGTTC
ACCACTTACCAGTCGCTGGACGCGATCCCTCGGGCTGAGCTGGCTCGC
CTGGAAAAGCGAGTTTTCCGCATGTCCATCGACGAGGT1TGGAACGA
AACCAAGCAGTTCTACGAGACCCGGCTCAACAACCCCGCCAAGGTTG
CCCGGGCGGAGCGCGACCCCAAGCTCAAGATGTCGCTCTGCTTTCGGT
GGTACTTGTCGAAAAGCTCCAAGTGGGCATCGACCTGGACAAGTTGGG
CGCGAGCTGGACTACCAGGTCTGGTGCGGCCCCACGATTGGCGCTTTC
AACGAGTTCGTGAAGGGGTCCAGCCTCGACGCGGAGGCTTGCGGGGG
GCGGTTTCCTTGCGTTGTGCGCGTTAACCAGGAGATATTATGTGGCGCT
GCTTACGAGCAGCGACTGGCGCGTTTCATGCTGCTCGCTGGCCGGGAA
AGCGCGGACGCGTTGGCGTACACGGTTGCGGAAGCCAGATAG

SEQ ID NO:10:
RKCIRPSLGHHWAIIGVLGRALRIVRPIRYEATNLRRLPRSGWLVALGLFCD
LSSCAGKLDLQTRDTAKDPCCKRKWSASRAPPRPRAEADKASNEMETKD
DRVAIVGMSAILPCGESVRESWEAIREGLDCLQDLPADRVDITAYYDPNKT
TKDKIYCKRGGFIPEYDFDAREFGLNMFQMEDSDANQTVTLLKVKEALED
AGVEPFTKKKKNIGCVLGIGGGQKASHEFYSRLNYVVVEKVLRKMNLPDE
VVEAAVEKYKANFPEWRLDSFPGFLGNVTAGRCSNVFMEGMNCVVDA
ACASSLIAIKVAIDELLHGDCDTMIAGATCTDNSIGMYMAFSKTPVFSTDQ
SVKAYDAKTKGMLIGEGSAMVVLKRYADAVRDGDEIHAVIRACASSSDGK

FIG.4-10

AAGIYAPTVSGQEEALRRAYARAGVDPSTVLVEGHGTGTPVGDRIELTAL
RNVFDAANKGRKETVAVGSIKSQIGHLKAVAGFAGLVKVVMALKHKTLP
QTINVHDPPALHDGSPIQDSSLYINTMNRPWFTAPGVPRRAGISSFGFGGA
NYHAVLEEAEPEHAKPYRMNQVPQPVLLHASSASALASICDAQADALQA
AVSPEASKHADYRAIVAFHEAFKLRAGVPAGHARIGFVSGSAAATLAVLR
AASAKLKQSSATLEWTLLREGVTYRSAAMHTPGSVAALFAGQGAQYTHM
FADVAMNWPPFRSAVQEMDAAQVTAAAPKRLSEVLYPRKPYAAEPEQD
NKAISMTINSQPALMACAAGAFEVFRQAGLAPDHVAGHSLGEFGALLAA
GCASREELFRLVCSRAKAMQDVPKPSEGVMAAVIGRGADKLTLQGDGAW
LANCNSPSQVVISGDKTAVERESSRLAGLGFRIIPLACEGAFHSPHMTAAQ
ATFQAALDSLKISTPTNGARLYNNVSGKTCRSLGELRDCLGKHMTSPVLFQ
AQVENMYAAGARIFVEFGPKQVLSKLVGEILADKSDFVTVAVNSSSSKDSD
VQLREAAAKLAVLGVPLANFDPWELCDARRLRECPRSKTTLRLSAATYVS
NKTLAAREKVMEDNCDFSSLFASGPASQEMEREIANLRAELEAAQRQLDT
AKTQLARKQVQDPTADRQRDMIAKHRSTLAAMVKEFEALASGSPCAVPF
APVVDTAVEDVPFADKVSTPPPQVTSAPIAELARAEAVVMEVLAAKTGYE
VDMIEADMLLDAELGIDSVKRIEILAAVQAQLGVEAKDVDALSRTRTVGE
VVDAMKAEIGGQATSAPSPMAQPQASAPSPSPTASVLPKPVALPASVDPA
KLARAEAVVMEVLAAKTGYEVDMIEADMLLDAELGIDSVKRIEILAAVQA
QLGVEAKDVDALSRTRTVGEVVDAMKAEIGGQATSAPASVAQPQASAPS
PSATTASVLPKPVAAPTSADPAKLARAEAVVMEVLAAKTGYEVDMIEAD
MLLDAELGIDSVKRIEILAAVQAQLGVEAKDVDALSRTRTVGEVVEAMKA
EIGGQATSAPASVAQPQISVSPTPLAASPSADPAKLARAEAVVMEVLAAKT
GYEVDMIEADMLLDAELGIDSVKRIEILAAVQAQLGVEAKDVDALSRTRT
VGEVVDAMKAEIGGQATSAPASVAQPQASAPSPSATASVLPKPVAAPTSA
DPAKLARAEAVVMEVLAAKTGYEVDMIEADMLLDAELGIDSVKRIEILAA
VQAQLGVEAKDVDALSRTRTVGEVVEAMKAEIGGQATSAPASMAQPSQIS
VSPTPLAASPSADPAKLARAEAVVMEVLAAKTGYEVDMIEADMLLDAEL
GIDSVKRIEILAAVQAQLGVEAKDVDALSRTRTVGEVVDAMKAEIGGQAT
SAPASVAQPQASAPSPSATASAPVTPLAAPASVDPAKLARAEAVVMEVLA
AKTGYEVDMIEADMLLDAELGIDSVKRIEILAAVQAQLGVEAKDVDALSR
TRTVGEVVDAMKAEIGGQATSAPASVAQPQASAPSPSATASVLPKPVASP
ASVDPAKLARAEAVVMEVLAAKTGYEVDMIDADMLLDAELGIDSVKRIEI
LAAVQAQLGVEAKDVDALSRTRTVGEVVEAMKAEIGAAGPNDAQAASG
HLFGTGCEDLSLCSASVVELARCSELALERPMDRPILIVSDGSALPAALASRL
GSCAVILTTAGETDQSVRSTKHVDMEGWGEADLVRALEAVESRFGVPGGV
VVLERASETARDQLGFALLLAKHSSKALNQQIPGGRACFVGVSRIDGKLGL
SGACAKGKGWAEAAEIAQQGAVAGLCKTLDLEWPHVFARSIDIELGANE
ETAAQAIFEELSCPDLTVREAGYTKDGKRWTTEARPVGLGKPKQALRSSDV
FLVSGGARGITPVCVRELAKSISGGTFVLLGRSPLADDPAWACGVEEANIG
TAAMAHLKAEFAAGRGPKPTPKAHKALVGSVLGAREVLGSLESIRAQGA
RAEYVSCDVSCAERVKAVVDDLERRVGAVTGVVHASGVLRDKSVERLELA
DFEVVYGTKVDGLLNLLQAVDRPKLRHLVLFSSLAGFHGNTGQAVYAMA
NEALNKMAFHLETAMPGLSVKTIGFGPWDGGMVNDALKAHFASMGVQI
IPLDGGAETVSRIIGACSPTQVLVGNWGLPPVVPNASVHKITVRLGGESAN

FIG.4-11

PFLSSHTIQGRKVLPMTVALGLLAEAARGLYVGHQVVGIEDAQVFQGVVL
DKGATCEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVVLGASG
PRTGGVQLELKDLGVDADPACSVGKGALYDGRTLFHGPAFQYMDEVLRC
SPAELAVRCRVVPSAAQDRGQFVSRGVLYDPFLNDTVFQALLVWARLVRD
SASLPSNVERISFHGQPPSEGEVFYTTLKLDSAASGPLDPIAKAQFFLHRAC
GAVFASGRASVVLNKALSF

SEQ ID NO:11:
QAIGHRAARWSCRSKSKARGHKAQKEMNQGGRNDEGVSVARADPCPDT
RIAVVGMAVEYAGCRGKEAFWDTLMNGKINSACISDDRLGSARREEHYA
PERSKYADTFCNERYGCIDPKVDNEHDLLLGLAAAALQDAQDRRSDGGK
FDPAQLKRCGIVSGCLSFPMDNLQGELLNLYQAHAERRIGKHCFADQTPW
STRTRALHPLPGDPRTHRDPASFVAGQLGLGPLHYSLDAACASALYVLRL
AQDHLLSGEADLMLCGATCFPEPFFILTGFSTFHAMPVGENGVSMPFHRD
TQGLTPGEGGSVMVLKRLADAERDGDHIYGTLLGASLSNAGCGLPLKHQ
PSEEACLKATYELVGVPPRDVQYVECHATGTPQGDTVELQAVKACFEGAS
PRIGSTKGNFGHTLVAAGFAGMCKVLLAMERGVIPPTPGVDSGTQIDPLV
VTAALPWPDTRGGPKRAGLSAFGF GGTNAHAVFEEHIPSRAPPAVLCQPR
LGSGPNRKLAIVGMDATFGSLKGLSALEAALYEARHAARPLPAKRWRFLG
GDESFLHEIGLECSPHGCYIEDVDVDFKRLRTPMVPEDLLRPQQLLAVSTID
KAILDSGLAKGGNVAVLVGLGTDLELYRHRARVALKERLQGLVRSAEGG
ALTSRLMNYINDSGTSTSYTSYIGNLVATRVSSQWGFTGPSFTVTEGANSVH
RCAQLAKYMLDRGEVDAVVVAGVDLCGSAEAFFVRSRRMQISKSQRPAA
PFDRAADGFFAGEGCGALVFKRLTDCVSGERIYASLDSVVVATTPRAALRA
AAGSARVDPASIDMVELSADSHRFVRAPGTVAQPLTAEVEVGAVREVIGT
AGRGSRSVAVGSVRANVGDAGFASGAAALVKTALCLHNRYLAATPGWD
APAAGVDFGAELYVCRESRAWVKNAGVARHAAISGVDEGGSCYGLVLSD
VPGQYETGNRISLQAESPKLLLLSAPDHAALLDKVAAELAALEQADGLSA
AAAAVDRLLGESLVGCAAGSGGLTLCLVASPASLHKELALAHRGIPRCIK
ARRDWASPAGSYFAPEPIASDRVAFMYGEGRSPYCGVGRDLHRIWPALHE
RVNAKTVNLWGDGDAWLLPRATSAEEEQLCRNFDSNQVEMFRTGVYIS
MCLTDLARSLIGLGPKASFGLSLGEVSMLFALSESNCRLSEEMTRRLRASPV
WNSELAVEFNALRKLWGVAPGAPVDSFWQGYVVRATRAQVEQAIGEDN
QFVRLLIVNDSQSVLIAGKPAACEAVIARIGSILPPLQVSQGMVGHCAEVLP
YTSEIGRIHNMLRFPSQDETGGCKMYSSVSNSRIGPVEESQMGPGTELVFSPS
MEDFVAQLYSRVADFPAITEAVYQQGHDVFVEVGPDHSRSAAVRSTLGPT
RRHIAVAMDRKGESAWSQLLKMLATLASHRVPGLDLSSMYHPAVVERCR
LALAAQRSGQPEQRNKFLRTIEVNGFYDPADATIPEAVATILPATAAISPPK
LGAPHDSQPEAEARPVGEASVPRRATSSSKLARTLAIDACDSDVRAALLDL
DAPIAVGGSSRAQVPPCPVSALGSAAFRAAHGVDYALYMGAMAKGVASA
EMVIAAGKARMLASFGAGGLPLGEVEEALDKIQAALPEGPFAVNLIHSPFD
PNLEEGNVELFLRRGIRLVEASAFMSVTPSLVRYRVAGLERGPGGTARVLN
RVIGKVSRAELAEMFMRPPPAAIVSKLLAQGLVTEEQASLAEIVPLVDDVAI
EADSGGHTDNRPIHVVLPVVLALRDRVMRECKYPAANRVRVGAGGGIGC
PAAARAAFDMGAAFVLTGSINQLTRQAGTSDSVRAALARATYSDVTMAP

FIG.4-12

AADMFDQGVKLQVLKRGTMFPARANKLYELFTTYQSLDAIPRAELARLEK
RVFRMSIDEVWNETKQFYETRLNNPAKVARAERDPKLKMSLCFRWYLSKS
SKWASTGQVGRELDYQVWCGPTIGAFNEFVKGSSLDAEACGGRFPCVVRV
NQEILCGAAYEQRLARFMLLAGRESADALAYTVAEAR

SEQ ID NO:12:
ATGGAGACAAAGGACGATCGCGTTGCGATCGTGGGCATGTCGGCCAT
ACTGCCTTGCGGTGAGTCAGTGCGCGAGTCGTGGGAGGCGATTCGCG
AGGGGCTCGATTGCCTGCAGGACCTGCCTGCGGACCGAGTCGATATC
ACGGCGTACTACGACCCGAACAAGACAACCAAGGACAAGATCTACT
GCAAGCGCGGCGGCTTCATTCCCGAGTATGACTTTGACGCGCGCGAGT
TCGGCCTCAACATGTTCCAGATGGAGGACTCGGACGCCAACCAAACC
GTGACTTTGCTCAAGGTCAAGGAGGCTCTCGAGGACGCCGGGGTGGA
GCCCTTCACAAAGAAGAAGAACATTGGCTGCGTGCTCGGCATCG
GCGGCGGGCAGAAGGCGAGCCACGAGTTTTACTCCCGACTCAACTAT
GTGGTCGTGGAGAAGGTGCTTCGCAAGATGAACCTCCCCGACGAGGT
TGTCGAGGCCGCCGTCGAAAAGTACAAGGCCAACTTTCCTGAATGGC
GCCTCGACTCGTTCCCTGGGTTTCTTGGCAACGTGACCGCCGGGCGGT
GCAGCAACGTCTTCAACATGGAAGGCATGAACTGCGTCGTGGACGCT
GCGTGCGCCAGCTCGCTCATCGCGATCAAGGTTGCCATTGATGAGCTC
CTCCACGGGGACTGCGACACCATGATTGCCGGTGCGACCTGCACCGA
CAACTCGATCGGGATGTACATGGCCTTTTCCAAAACCCCAGTTTTCTCC
ACCGACCAGAGCGTCAAGGCGTACGACGCCAAGACGAAAGGCATGC
TCATCGGCGAAGGCTCGGCCATGGTCGTGCTCAAGCGGTACGCGGAC
GCCGTTCGGGATGGTGATGAGATCCATGCCGTCATCAGGGCATGCGCC
TCGTCCAGCGACGGCAAGGCTGCTGGCATTTACGCACCGACGGTGTCG
GGTCAAGAAGAGGCACTGCGGCGCGCGTACGCCCGAGCTGGCGTGGA
CCCCTCCACCGTCACGCTGGTGGAGGGCCACGGCACTGGCACACCCG
TCGGGGACCGGATTGAGCTGACCGCCTTGCGCAACGTCTTTGACGCAG
CCAACAAAGGCCGCAAGGAAACAGTCGCGGTGGGAAGCATCAAGTC
GCAGATCGGTCACCTGAAGGCCGTGGCCGGCTTTGCCGGTCTCGTCAA
GGTTGTCATGGCCCTCAAGCACAAGACGCTGCCGCAGACCATCAACG
TTCACGACCCGCCCGCACTGCACGACGGCTCGCCCATCCAGGATTCGA
GTCTTTACATCAACACGATGAACCGGCCCTGGTTTACGGCACCTGGCG
TCCCCCGCCGTGCAGGCATCTCTAGCTTTGGGTTTGGCGGCGCCAACT
ACCACGCTGTTCTCGAAGAGGCCGAGCCTGAGCACGCGAAGCCGTAT
CGCATGAACCAAGTTCCACAACCGGTGCTCTTGCACGCAAGCTCCGCG
TCAGCTCTT

SEQ ID NO:13:
METKDDRVAIVGMSAILPCGESVRESWEAIREGLDCLQDLPADRVDITAYY
DPNRGGFIPEYDFDAREFGLNMFQMEDSDANQTVTLLKVKEALEDAGVEP
FTK
KKKNIGCVLGIGGGQKASHEFYSRLNYVVVEKVLRKMNLPDEVVEAAVEK
YKANFPEWRLDSFPGFLGNV TAGRCSNVFN

FIG.4-13

MEGMNCVVDAACASSLIAIK
VAIDELLHGDCDTMIAGATCTDNSIGMYMAFSKTPVFSTDQSVKAYDAKT
KGMLIGEGSAMVVLKRYADAVRDGDEIHAVIRACASSSDGKAAGIYAPTV
SGQEEALRRAYARAGVDPSTVTLVEGHGTGTPVGDRIELTALRNVFDAAN
KGRKETVAVG SIKSQIGHLK
AVAGFAGLVKVVMALKHKTLPQTINVHDPP
ALHDGSPIQDSSLYINTMNRPWFTAPGVPRRAGISSFGFGGANYHAVLEE
AEPEHAKPYRMNQVPQPVLLHASSASAL

SEQ ID NO:14:
CAGTCGAGTGCGACGCTCGAATGGACCCTGCTCCGCGAGGGCGTCAC
GTACCGCTCCGCCGCGATGCACACTCCTGGCAGTGTCGCTGCTCTGTTT
GCCGGGCAAGGCGCGCAGTACACGCACATGTTCGCTGACGTTGCCAT
GAACTGGCCACCGTTTCGAAGCGCCGTGCAAGAGATGGATGCCGCTC
AAGTCACGGCGGCAGCGCCGAAGCGCCTCAGCGAGGTCCTGTATCCG
CGCAAGCCGTACGCTGCAGAGCCCGAGCAAGACAACAAGGCCATCTC
GATGACGATTAACTCGCAACCGGCCCTCATGGCCTGCGCTGCTGGGGC
GTTTGAGGTGTTTCGTCAAGCTGGTCTTGCGCCCGACCACGTCGCGGG
TCATTCTCTCGGCGAGTTTGGTGCTTTGCTCGCCGCTGGATGCGCAAGC
CGTGAGGAGCTCTTCCGTCTGGTCTGCAGCAGAGCGAAGGCAATGCA
AGACGTTCCCAAGCCAAGCGAGGGCGTCATGGCAGCTGTCATCGGCC
GTGGTGCTGACAAGCTCACGCTGCAAGGCGATGGTGCGTGGCTTGCCA
ACTGCAACTCGCCAAGCCAAGTGGTCATTTCCGGCGACAAGACTGCT
GTCGAGCGTGAATCCAGCCGGTTGGCAGGCCTTGGCTTCAGGATCATT
CCGCTTGCATGCGAAGGCGCCTTCCATTCACCGCACATGACGGCGGCC
CAGGCCACGTTTCAGGCTGCACTGGACAGCCTCAAGATCTCCACCCCG
ACGAACGGGGCGCGCCTGTACAACAACGTTTCCGGAAAGACCTGCCG
ATCCCTGGGTGAACTCCGCGACTGCCTGGGCAAGCACATGACAAGTC
CTGTGCTCTTCCAGGCACAGGTAGAGAACATGTACGCTGCCGGGGCG
CGCATTTTCGTGGAGTTTGGCCCGAAGCAAGTCCTCTCCAAGCTCGTA
GGCGAGATTCTCGCCGACAAGTCAGACTTTGTGACAGTCGCGGTCAAC
TCGTCATCGTCCAAGGACAGCGACGTGCAACTTCGTGAAGCTGCTGCG
AAGCTCGCGGTCCTTGGCGTCCCGTTGGCGAACTTTGACCCTTGGGAG
CTCTGCGACGCGCGGCGTCTTCGCGAATGCCCGCGATCCAAGACGAC
GTTGCGCTTGTCTGCAGCGACCTACGTGTCGAACAAGACCCTTGCTGC
TAGGGAGAAGGTCATGGAGGACAACTGCGACTTTTCTTCGCTCTTTGC
CTCCGGTCCAGCAAGCCAAGAGATGGAGCGAGAAATAGCCAACCTTC
GCGCTGAGCTGGAGGCGGCCCAACGCCAGCTTGACACGGCCAAA

SEQ ID NO:15:
QSSATLEWTLLREGVTYRSAAMHTPGSVAALFAGQGAQYTHMFADVAM
NWPPFRSAVQEMDAAQVTAAAPKRLSEVLYPRKPYAAEPEQDNKAISMTI
NSQPALMACAAGAFEVFRQAGLAPDHVAGHSLGEFGALLAAGCASREEL
FRLVCSRAKAMQDVPKPSEGVMAAVIGRGADKLTLQGDGAWLANCNSP
SQVVISGDKTAVERESSRLAGLGFRIIPLACEGAFHSPHMTAAQATFQAAL

FIG.4-14

DSLKISTPTNGARLYNNVSGKTCRSLGELRDCLGKHMTSPVLFQAQVENM
YAAGARIFVEFGPKQVLSKLVGEILADKSDFVTVAVNSSSSKDSDVQLREA
AAKLAVLGVPLANFDPWELCDARRLRECPRSKTTLRLSAATYVSNKTLAA
REKVMEDNCDFSSLFASGPASQEMEREIANLRAELEAAQRQLDTAK

SEQ ID NO:16:
CAAGTCACTTCCGCTCCCATCGCCGAGCTCGCGCGCGCCGAGGCCGTC
GTCATGGAGGTTCTCGCTGCCAAGACTGGCTACGAGGTCGACATGATC
GAGGCCGACATGCTGCTCGACGCCGAGCTCGGCATCGACTCGGTCAA
GCGCATTGAGATCCTGGCAGCTGTCCAGGCCCAGCTCGGGGTCGAGG
CCAAGGACGTCGACGCGCTCAGCCGCACACGAACAGTTGGCGAGGTC
GTTGACGCCATGAAGGCTGAGATCGGCGGG

SEQ ID NO:17:
QVTSAPIAELARAEAVVMEVLAAKTGYEVDMIEADMLLDAELGIDSVKRIE
ILAAVQAQLGVEAKDVDALSRTRTVGEVVDAMKAEIGG

SEQ ID NO:18:
CATCTCTTTGGCACGGGATGTGAAGACCTGAGCCTTTGCTCTGCTTCTG
TGGTTGAGATTGCTCGTTGCAGCGAACTAGCTCTGGAGCGCCCGATGG
ATCGGCCCATTCTTATTGTAAGCGATGGATCAGCATTGCCGGCGGCTC
TGGCTAGTCGACTGGGGTCGTGTGCAGTAATCCTCACGACCGCAGGCG
AGACCGACCAATCTGTGCGCTCGACGAAGCACGTTGACATGGAAGGG
TGGGGCGAGGCAGATCTCGTGCGCGCTCTTGAAGCAGTAGAGTCTCG
ATTCGGCGTCCCAGGCGGCGTCGTGGTGCTTGAGCGCGCCTCAGAAAC
AGCTAGGGACCAGCTTGGCTTTGCCCTGCTGCTTGCCAAGCATTCGAG
CAAAGCGCTCAACCAGCAGATCCCAGGCGGGCGCGCCTGCTTCGTGG
GCGTCTCGCGAATCGACGGAAAGCTCGGACTTAGCGGAGCTTGCGCG
AAAGGAAAGGGCTGGGCTGAGGCCGCAGAGATTGCTCAGCAAGGAG
CCGTCGCGGGCTTGTGCAAGACCTTGGACCTAGAGTGGCCGCACGTCT
TCGCTCGCAGCATCGACATCGAGCTTGGCGCGAACGAAGAAACAGCT
GCGCAAGCAATCTTTGAGGAGCTCTCTTGCCCGGACCTAACGGTGCGC
GAAGCAGGATACACCAAAGACGGCAAGCGGTGGACGACTGAGGCGC
GACCGGTTGGGCTTGGCAAGCCCAAGCAGGCACTACGTTCTTCGGAC
GTCTTCTTGGTTTCTGGTGGGGCGCGGGGAATTACACCTGTTTGCGTTC
GCGAGTTGGCCAAATCGATCAGTGGTGGCACTTTTGTCCTCCTCGGGC
GGTCCCCTCTCGCTGATGATCCGGCGTGGGCTTGCGGCGTCGAGGAAG
CAAACATTGGGACAGCCGCTATGGCGCACCTCAAGGCCGAGTTCGCA
GCCGGGCGCGGCCCGAAGCCGACGCCAAAGGCCCACAAAGCACTCG
TTGGGAGCGTCCTGGGGGCGCGCGAAGTCCTTGGTTCGCTAGAGAGTA
TTCGCGCCCAGGGTGCGCGCGCCGAGTACGTTTCCTGCGACGTTTCGT
GTGCGGAGCGCGTCAAGGCCGTCGTCGACGATCTCGAGCGACGGGTC
GGGGCTGTAACTGGGGTTGTGCACGCCTCTGGTGTTCTCCGAGACAAG
TCCGTTGAGCGCTTGGAGCTCGCCGACTTCGAGGTCGTGTACGGCACC
AAGGTGGACGGCCTGCTCAACCTGCTGCAGGCCGTGGACCGCCCCAA

FIG.4-15

ACTCCGGCACTTGGTCCTCTTCAGCTCCCTGGCCGGTTTCCACGGCAAC
ACTGGGCAGGCCGTGTACGCTATGGCGAATGAGGCGCTGAACAAGAT
GGCCTTCCATTTGGAAACTGCGATGCCTGGCCTCTCGGTCAAGACGAT
CGGGTTTGGACCTTGGGACGGCGGCATGGTCAACGATGCGCTGAAAG
CGCACTTTGCGTCTATGGGCGTCCAAATTATTCCGCTCGACGGCGGCG
CGGAGACCGTTTCCCGAATCATCGGGGCGTGCTCGCCAACACAAGTTC
TGGTTGGCAACTGGGGCTTGCCCCCTGTAGTTCCTAACGCGAGCGTGC
ACAAGATTACTGTGAGGCTTGGCGGGGAGTCTGCAAACCCTTTCCTGT
CCTCGCACACGATTCAAGGCAGAAAGGTCTTGCCGATGACTGTGGCG
CTTGGGCTTCTCGCTGAGGCGGCTCGAGGGCTCTACGTCGGTCACCAA
GTAGTCGGGATTGAGGACGCCCAAGTCTTCCAGGGAGTCGTGTTGGAC
AAAGGGGCGACGTGTGAGGTCCAGCCGCCGCGAGTCTTCGACTGC
AAGCCCAAGCGAGGTTGTGCTGAGTGCTTCGCTCAATGTATTCGCGGC
GGGAAAGGTTGTGCCTGCGTACCGCGCGCATGTCGTGCTCGGCGCTTC
AGGGCCACGCACTGGCGGCGTGCAGCTTGAACTGAAAGATTTGGGCG
TGGACGCCGACCCTGCTTGCTCCGTTGGCAAGGGTGCGCTGTACGACG
GTAGGACGCTGTTCCATGGGCCGGCGTTTCAGTACATGGATGAGGTTC
TTCGGTGCTCGCCTGCAGAGCTTGCCGTGCGGTGCCGTGTCGTTCCGA
GCGCGGCTCAGGACCGCGGCCAATTTGTTTCGCGCGGAGTGTTGTACG
ACCCGTTCCTGAACGACACGGTGTTTCAAGCTCTCCTTGTTTGGGCCCG
TCTGGTCAGGGACAGCGCTTCGCTACCGAGCAACGTTGAACGAATCTC
GTTCCACGGCCAGCCGCCGAGCGAGGGCGAGGTGTTTTACACCACGC
TCAAGCTGGACAGTGCTGCGAGCGGGCCGCTCGACCCGATTGCAAAG
GCGCAGTTCTTCCTCCACCGAGCTTGCGGGGCGGTCTTTGCATCAGGG
CGAGCGAGTGTGGTTCTGAACAAGGCTCTTTCGTTT

SEQ ID NO:19:
ASGHLFGTGCEDLSLCSASVVEIARCSELALERPMDRPILIVSDGSALPAAL
ASRLGSCAVILTTAGETDQSVRSTKHVDMEGWGEADLVRALEAVESRFGV
PGGVVVLERASETARDQLGFALLLAKHSSKALNQQIPGGRACFVGVSRIDG
KLGLSGACAKGKGWAEAAEIAQQGAVAGLCKTLDLEWPHVFARSIDIEL
GANEETAA
QAIFEELSCPDLTVREAGYTKDGKRWTTEARPVGLGKPKQALRSSDVFLV
SGGARGITPVCVRELAKSISGGTFVLLGRSPLADDPAWACGVEEANIGTA
AMAHLKAEFAAGRGPKPTPKAHKALVGSVLGAREVLGSLESIRAQGARA
E
YVSCDVSCAERVKAVVDDLERRVGAVTGVVHASGVLRDKSVERLELADFE
VVYGTKVDGLLNLLQAVDRPKLRHLVLFSSLAGFHGNTGQAVYAMANE
AL
NKMAFHLETAMPGLSVKTIGFGPWDGGMVNDALKAHFASMGVQIIPLDG
G
AETVSRTIGACSPTQVLVGNWGLPPVVPNASVHKITVRLGGESANPFLSS
HTIQGRKVLPMTVALGLLAEAARGLYVGHQVVGIEDAQVFQGVVLDKGA
T
CEVQLRRESSTASPSEVVLSASLNVFAAGKVVPAYRAHVVLGASGPRTGG

FIG.4-16

VQLELKDLGVDADPACSVGKGALYDGRTLFHGPAFQYMDEVLRCSPAEL
A
VRCRVVPSAAQDRGQFVSRGVLYDPFLNDTVFQALLVWARLVRDSASLPS
NVERISFHGQPPSEGEVFYTTLKLDSAASCPLDPIAKAQFFLHRACGAVF
ASGRASVVLNKALSF

SEQ ID NO:20:
ATGAACCAGGGCGGGAGAAATGACGAGGGCGTCTCGGTGGCGCGCGCG
GACCCATGCCCTGACACGCGGATCGCTGTCGTGGGCATCGCGGTCGAGTA
TGCAGGGTGCCGCGGCAAGGAAGCGTTCTGGGACACGCTCATGAACGGC
AAAATCAACTCTGCCTGTATCTCAGACGATCGCCTCGGGTCAGCACGACG
AGAAGAGCACTATGCGCCCGAGAGGTCAAAGTACGCCGATACGTTCTGC
AACGAGAGGTACGGATGCATCGATCCCAAAGTCGACAACGAGCACGAC
CTGCTCCTCGGCCTCGCCGCGGCTGCGCTTCAAGACGCGCAGGACAGGCG
CAGCGACGGCGGCAAGTTCGACCCAGCGCAGCTCAAGCGCTGCGGCATT
GTCAGCGGCTGCCTGTCCTTCCCGATGGACAACCTGCAAGGCGAGCTGCT
CAACCTTTACCAAGCCCATGCTGAGAGGCGGATTGGCAAGCATTGCTTCG
CGGACCAAACGCCCTGGTCGACGCGAACCAGAGCGCTTCACCCGCTGCC
CGGGGACCCGAGGACCCACCGCGACCCAGCCTCCTTCGTCGCCGGACAG
CTCGGCCTCGGCCCGCTGCACTACTCGCTCGACGCCGCCTGCGCCTCGGC
CCTTTACGTTCTGCGACTCGCTCAGGACCACCTCCTCTCGGGCGAGGCTG
ACTTGATGCTGTGCGGAGCGACGTGCTTCCCAGAGCCCTTCTTCATCCTGA
CTGGGTTTAGCACGTTCCACGCGATGCCAGTCGGTGAGAACGGTGTCTCG
ATGCCGTTTCATCGGGACACGCAAGGGCTGACGCCCGGCGAGGGCGGCT
CGGTGATGGTGCTCAAGCGCCTCGCGGACGCCGAGCGCGACGGAGACCA
CATCTACGGGACGCTTCTTGGAGCCAGCTTGAGCAACGCAGGCTGCGGG
CTTCCTCTCAAGCCGCACCAGCCAAGCGAGGAGGCCTGCTTGAAAGCCA
CCTACGAGCTCGTCGGCGTGCCGCCCCGAGACGTCCAGTACGTCGAGTGC
CACGCCACCGGCACGCCGCAGGGCGACACCGTCGAGCTCCAAGCCGTCA
AAGCCTGCTTTGAGGGCGCAAGCCCCCGGATCGGGTCCACGAAAGGCAA
CTTCGGACACACCCTCGTCGCGGCCGGCTTTGCGGGAATGTGCAAGGTTC
TCCTTGCAATGGAGCGCGGCGTGATCCCCCCGACCCCGGGCGTTGACTCT
GGCACCCAGATTGATCCCCTCGTCGTCACAGCGGCGCTCCCGTGGCCGGA
TACGCGCGGCGGGCCGAAACGCGCAGGACTCTCCGCATTCGGATTCGGG
GGCACAAACGCGCACGCCGTCTTTGAGGAGCATATTCCCTCGAGAGCT

SEQ ID NO:21:
MNQGGRNDEGVSVARADPCPDTRIAVVGMAVEYAGCRGKEAFWDTLMNG
KINSACISDDRLGSARREEHYAPERSKYADTFCNERYGCIDPKVDNEHDLLLG
LAAAALQDAQDRRSDGGKFDPAQLKRCGIVSGCLSFPMDNLQGELLNLYQA
HAERRIGKHCFADQTPWSTRTRALHPLGDPRTHRDPASFVAGQLGLGPLHY
SLDAACASALYVLRLAQDHLLSGEADLMLCGATCFPEPFFILTGFSTFHAMPV
GENGVSMPFHRDTQGLTPGEGGSVMVLKRLADAERDGDHIYGTLLGASLSN
AGCGLPLKPHQPSEEACLKATYELVGVPPRDVQYVECHATGTPQGDTVELQA
VKACFEGASPRIGSTKGNFGHTLVAAGFAGMCKVLLAMERGVIPPTPGVDSG

FIG.4-17

TQIDPLVVTAALPWPDTRGGPKRAGLSAFGFGGTNAHAVFEEHIPSRA

SEQ ID NO: 22:

CAGCCTCGCCTCGGCAGCGGACCAAACCGAAAGCTTGCTATCGTCGGCA
TGGATGCCACGTTTGGATCCTTGAAGGGTCTCTCCGCACTAGAAGCTGCG
CTTTACGAGGCAAGGCACGCTGCGCGGCCCCTGCCTGCGAAGCGCTGGC
GCTTCTTGGGCGGGGACGAGTCCTTTCTCCACGAGATCGGACTCGAGTGC
TCTCCGCACGGGTGCTACATTGAGGACGTGGATGTGGACTTTAAGCGACT
CCGCACGCCAATGGTGCCGGAGGACTTGCTCCGGCCGCAACAGCTCCTG
GCCGTGTCGACGATTGACAAGGCCATCCTCGACTCGGGCTTGGCCAAGG
GCGGCAACGTGGCTGTCCTTGTCGGCCTCGGGACGGACCTCGAGCTCTAC
CGCCACCGAGCTCGGGTTGCGCTTAAGGAGCGTCTTCAAGGACTGGTTCG
CTCTGCCGAGGGAGGAGCCCTGACGTCTCGCCTGATGAACTATATCAATG
ATAGCGGAACGTCGACCTCCTACACGTCGTATATCGGCAACCTCGTCGCC
ACGCGCGTCTCGTCCCAGTGGGGCTTCACTGGGCCGTCGTTCACCGTCAC
GGAAGGGGCCAACTCGGTCCATCGGTGCGCCCAGCTCGCCAAGTACATG
CTCGACCGCGGCGAGGTCGACGCCGTCGTGGTTGCAGGAGTCGACCTGTG
CGGGAGCGCCGAGGCGTTCTTCGTGAGGTCGCGCCGCATGCAGATCTCGA
AAAGTCAGCGCCCGGCCGCGCCGTTTGACCGCGCCGCAGACGGCTTCTTC
GCGGGGGAAGGGTGCGGCGCCCTCGTCTTCAAACGCCTGACTGACTGTGT
GTCTGGCGAGCGAATCTACGCGTCCCTCGACTCGGTCGTCGTCGCAACCA
CGCCGCGCGCCGCTCTTCGTGCTGCCGCAGGGTCGGCGCGGGTTGACCCA
GCCAGCATCGACATGGTCGAGCTGAGCGCAGATTCCCACCGGTTTGTGCG
GGCGCCAGGCACCGTGGCTCAGCCTCTGACAGCCGAAGTCGAGGTCGGG
GCGGTGCGGGAAGTGATCGGGACCGCGGGGAGGGGCTCTCGAAGCGTGG
CCGTCGGATCGGTCCGCGCCAACGTCGGGGACGCAGGGTTTGCTTCCGGG
GCCGCTGCCCTCGTAAAAACTGCGCTCTGCTTGCACAACCGCTACTTGGC
GGCTACCCCAGGCTGGGATGCGCCTGCTGCCGGCGTGGATTTTGGTGCCG
AGCTGTACGTTTGCCGCGAGTCGCGTGCTTGGGTCAAGAACGCCGGCGTT
GCACGGCACGCCGCAATTTCTGGCGTGGACGAAGGCGGGTCG

SEQ ID NO:23:
QPRLGSGPNRKLAIVGMDATFGSLKGLSALEAALYEARHAARPLPAKRWRFL
GGDESFLHEIGLECSPHGCYIEDVDVDFKRLRTPMVPEDLLRPQQLLAVSTIDK
AILDSGLAKGGNVAVLVGLGTDLELYRHRARVALKERLQGLVRSAEGGALTS
RLMNYINDSGTSTSYTSYIGNLVATRVSSQWGFTGPSFTVTEGANSVHRCAQL
AKYMLDRGEVDAVVAGVDLCGSAEFFVRSRRMQISKSQRPAAPFDRAAD
GFFAGEGCGALVFKRLTDCVSGERIYASLDSVVVATTPRAALRAAAGSARVDP
ASIDMVELSADSHRFVRAPGTVAQPLTAEVEVGAVREVIGTAGRGSRVAVGS
VRANVGDAGFASGAAALVKTALCLHNRYLAATPGWDAPAAGVDFGAELYV
CRESRAWVKNAGVARHAAISGVDEGGS

SEQ ID NO:24:
TGCTATGGGCTGGTTCTTTCGGACGTGCCTGGCAGTACGAGACCGGCAA

FIG.4-18

CCGCATCTCCCTCCAGGCCGAGTCGCCCAAGCTCTTGCTCCTCTCGGTCC
AGACCACGCCGCCTTGCTGGACAAGGTGGCGGCCGAGCTCGCAGCCCTT
GAGCAAGCCGACGGCTTGAGCGCCGCCGCGGCTGCCGTAGACCGCTTAC
TCGGCGAGTCGCTCGTCGGTTGCGCGGCTGGCAGCGGCGGGCTGACCCTT
TGCTTGGTGGCTTCGCCTGCCAGCCTCCACAAGGAGCTTGCGCTGGCCCA
TCGAGGGATCCCGCGCTGCATCAAAGCACGGCGCGACTGGGCCAGCCCG
GCAGGGAGCTACTTCGCCCCGGAGCCGATCGCAAGCGACCGCGTCGCGT
TCATGTACGGGGAAGGACGAAGCCCGTACTGCGGCGTCGGCCGCGACCT
CCACCGGATCTGGCCCGCGCTGCATGAGCGGGTGAACGCCAAGACTGTC
AACCTCTGGGGTGACGGTGACGCCTGGCTGCTGCCACGTGCAACCTCGGC
CGAGGAAGAGGAGCAACTCTGCCGCAACTTCGACTCGAACCAGGTTGAG
ATGTTTCGAACGGGCGTGTACATCTCGATGTGCTTGACCGACCTCGCTCG
AAGCTTGATTGGACTGGGCCCTAAGGCGAGCTTTGGGCTCAGCCTAGGCG
AGGTTTCCATGCTCTTCGCTCTGAGCGAGTCCAACTGTAGACTGTCGGAG
GAAATGACCCGCAGGCTCCGTGCGTCCCGGTGTGGAACTCGGAGCTCG
CCGTCGAGTTCAACGCCCTTCGAAAGTTGTGGGGGGTCGCGCCGGGGGC
ACCCGTCGACTCGTTCTGGCAAGGTTATGTCGTGCGCGCAACGCGGGCTC
AGGTGGAGCAAGCCATTGGGGAGGACAATCAGTTTGTGCGTCTCCTGATC
GTGAACGACTCGCAATCAGTCCTGATCGCCGGCAAGCCGGCGGCGTGCG
AAGCCGTAATTGCTCGCATCGGGTCTATTCTTCCCCCGCTGCAAGTGTCGC
AAGGCATGGTGGGGCACTGTGCCGAGGTCTTGCCGTACACGAGCGAGAT
CGGGCGCATCCACAACATGCTTCGCTTCCCATCGCAGGACGAAACGGGC
GGTTGCAAAATGTACTCTAGCGTCTCAAACTCGCGCATCGGGCCAGTCGA
GGAGAGCCAGATGGGCCCAGGCACTGAGCTCGTTTTCTCGCCGTCAATGG
AAGACTTTGTCGCCCAGCTGTACTCGCGAGTTGCAGACTTTCCGGCGATC
ACCGAGGCGGTTTACCAGCAGGGTCATGACGTGTTTGTCGAAGTGGGGCC
GGACCATTCACGGTCGGCTGCTGTCCGCTCCACGCTTGGACCCACTCGGC
GACACATCGCTGTGGCGATGGACCGCAAGGGTGAGTCAGCTTGGTCGCA
GCTTCTGAAAATGCTGGCTACGCTTGCGTCGCACCGCGTGCCGGGCCTG

SEQ ID NO:25:
CYGLVLSDVPGQYETGNRISLQAESPKLLLLSAPDHAALLDKVAAELAALEQA
DGLSAAAAAVDRLLGESLVGCAAGSGGLTLCLVASPASLHKELALAHRGIPR
CIKARRDWASPAGSYFAPEPIASDRVAFMYGEGRSPYCGVGRDLHRIWPALHE
RVNAKTVNLWGDGDAWLLPRATSAEEEEQLCRNFDSNQVEMFRTGVYISMC
LTDLARSLIGLGPKASFGLSLGEVSMLFALSESNCRLSEEMTRRLRASPVWNSEL
AVEFNALRKLWGVAPGAPVDSFWQGYVVRATRAQVEQAIGEDNQFVRLLIV
NDSQSVLIAGKPAACEAVIARIGSILPPLQVSQGMVGHCAEVLPYTSEIGRIHN
MLRFPSQDETGGCKMYSSVSNSRIGPVEESQMGPGTELVFSPSMEDFVAQLYSR
VADFPAITEAVYQQGHDVFVEVGPDHSRSAAVRSTLGPTRRHIAVAMDRKGE
SAWSQLLKMLATLASHRVPGL

SEQ ID NO:26:
GCGACCATCCCTGAGGCCGTCGCAACAATTCTGCCGGCAACTGCTGCGAT
TTCGCCTCCAAAGCTTGGCGCTCCGCACGACTCGCAACCCGAGGCGGAG

FIG.4-19

GCTCGCCCCGTGGGCGAGGCCTCTGTGCCAAGGCGGGCCACGAGCTCGA
GCAAATTGGCCAGGACGCTTGCCATCGATGCTTGCGACTCCGACGTGCGC
GCCGCCTTGCTGGACCTGGACGCGCCAATCGCGGTCGGCGGCTCCTCGCG
CGCCCAAGTCCCGCCGTGCCCAGTGAGCGCGCTCGGAAGCGCCGCCTTTC
GAGCGGCACACGGCGTCGATTATGCGCTCTACATGGGCGCAATGGCCAA
AGGCGTCGCGTCAGCGGAGATGGTCATCGCTGCTGGCAAGGCCCGCATG
CTCGCGTCATTTGGCGCGGGGGGGCTTCCCCTGGGCGAGGTCGAAGAGGC
GTTGGACAAGATCCAGGCCGCTCTGCCCGAGGGGCCGTTCGCCGTCAACC
TCATTCACTCGCCGTTCGATCCAAACCTTGAGGAGGGCAACGTCGAGCTG
TTCCTGAGGCGCGGTATCCGGCTGGTCGAGGCCTCTGCGTTCATGTCGGTC
ACGCCGTCGTTGGTGCGCTACCGAGTCGCCGGACTCGAGCGAGGCCTG
GCGGGACCGCCCGAGTGCTGAACCGCGTGATTGGCAAGGTGAGCCGTGC
GGAGCTCGCAGAAATGTTTATGCGGCCGCCTCCCGCCGCGATCGTCTCCA
AGCTCCTCGCCCAGGGCCTGGTCACTGAGGAGCAGGCGTCACTTGCAGA
GATCGTCCCACTGGTTGACGACGTTGCAATCGAAGCCGACTCGGGCGGTC
ACACAGACAACCGCCCGATCCACGTCGTTTTGCCCGTCGTCCTCGCGCTG
CGAGACCGCGTCATGCGTGAGTGCAAGTATCCAGCCGCCAATCGCGTCC
GCGTGGGCGCCGGAGGCGGGATCGGCTGCCCTGCCGCGGCGCGAGCTGC
GTTCGACATGGGCGCAGCATTCGTTCTCACGGGCTCGATCAACCAGCTCA
CGCGCCAGGCTGGGACGAGCGACAGCGTGCGTGCTGCCCTTGCACGCGC
GACCTACTCGGACGTGACAATGGCCCCGGCGGCCGATAGTTTGACCAG
GGCGTCAAGCTGCAGGTCTTGAAGCGCGGCACGATGTTCCCGGCGCGCG
CAAACAAGCTGTACGAGTTGTTCACCACTTACCAGTCGCTGGACGCGATC
CCTCGGGCTGAGCTGGCTCGCCTGGAAAAGCGAGTTTTCCGCATGTCCAT
CGACGAGGTTTGGAACGAAACCAAGCAGTTCTACGAGACCCGGCTCAAC
AACCCCGCCAAGGTTGCCCGGGCGGAGCGCGACCCCAAGCTCAAGATGT
CGCTCTGCTTTCGGTGGTACTTGTCGAAAAGCTCCAAGTGGGCATCGACT
GGACAAGTTGGGCGCGAGCTGGACTACCAGGTCTGGTGCGGCCCCACGA
TTGGCGCTTTCAACGAGTTCGTGAAGGGGTCCAGCCTCGACGCGGAGGCT
TGCGGGGGGCGGTTTCCTTGCGTTGTGCGCGTTAACCAGGAGATATTATG
TGGCGCTGCTTACGAGCAGCGACTGGCGCGTTTCATGCTGCTCGCTGGCC
GGGAAAGCGCGGACGCGTTGGCGTACACGGTTGCGGAAGCCAGATAG

SEQ ID NO:27:
ATIPEAVATILPATAAISPPKLGAPHDSQPEAEARPVGEASVPRRATSSSKLART
LAIDACDSDVRAALLDLDAPIAVGGSSRAQVPPCPVSALGSAAFRAAHGVDY
ALYMGAMAKGVASAEMVIAAGKARMLASFGAGGLPLGEVEEALDKIQAALP
EGPFAVNLIHSPFDPNLEEGNVELFLRRGIRLVEASAFMSVTPSLVRYRVAGLE
RGPGGTARVLNRVIGKVSRAELAEMFMRPPPAAIVSKLLAQGLVTEEQASLAE
IVPLVDDVAIEADSGGHTDNRPIHVVLPVVLALRDRVMRECKYPAANRVRVG
AGGGIGCPAAARAAFDMGAAFVLTGSINQLTRQAGTSDSVRAALARATYSDV
TMAPAAMFDQGVKLQVLKRGTMFPARANKLYELFTTYQSLDAIPRAELARL
EKRVFRMSIDEVWNETKQFYETRLNNPAKVARAERDPKLKMSLCFRWYLSKS
SKWASTGQVGRELDYQVWCGPTIGAFNEFVKGSSLDAEACGGRFPCVVRVN
QEILCGAAYEQRLARFMLLAGRESADALAYTVAEAR

FIG.4-20